





XX 07-AUG-2000 (first entry)  
 XX NCAM Igl binding peptide 120 used as a control peptide.  
 DE NCAM: neural cell adhesion molecule, Ig1, immunoglobulin domain 1;  
 XX neurite outgrowth promoter; proliferation; nerve damage; sclerosis;  
 KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;  
 KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;  
 XX treatment; prosthetic nerve guide; treatment; nervous system.  
 XX Synthetic.  
 OS  
 XX WO200018801-A2.  
 PN  
 XX 06-APR-2000.  
 PD  
 XX 23-SEP-1999; 99WO-DK00500.  
 FE  
 XX 29-SEP-1999; 99FR-0001332.  
 PR 29-APR-1999; 99PK-0000592.  
 XX (RONN/) RONN L C B.  
 PA (BOCK/) BOCK E.  
 PA (HOLM/) HOLM A.  
 PA (OLSE/) OLSEN M.  
 PA (OSTE/) OSTERGAARD S.  
 PA (JENS/) JENSEN P H.  
 PA (POUL/) POULSEN F M.  
 PA (SORO/) SOROKA V.  
 PA (RALE/) RALETS I.  
 PA (BERE/) BEREZIN V.  
 XX Poulson LCB, Rock E, Holm A, Olsen M, OSTERGAARD S, Jensen PH;  
 PI Poulson FM, Soroka V, Ralets I, Berezin V;  
 XX WPI: 2000-293111/25.  
 XX Compositions that bind neural cell adhesion molecules useful for  
 PT treating disorders of the nervous system and muscles e.g. Alzheimer's  
 PT and Parkinson's diseases -  
 XX Example 5; Fig 7; 11pp; English.  
 XX Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.  
 CC NCAM is found in three forms, two of which are transmembrane forms, while  
 CC the third is attached via a lipid anchor to the cell membrane. All three  
 CC NCAM forms have an extracellular structure consisting five immunoglobulin  
 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the  
 CC N-terminal. The invention relates to a compound containing a peptide  
 CC which binds to the NCAM Igl domain. The compound binds to NCAM-Igl/Ig2  
 CC domain, and is capable of stimulating or promoting neurite outgrowth  
 CC from NCAM presenting cells, and is also capable of promoting the  
 CC proliferation of NCAM presenting cells. The present sequence represents a  
 CC peptide used in the identification of those binding peptides  
 CC which can be used in the compound. The compound may be used in the  
 CC treatment of normal, degenerated or damaged NCAM presenting cells. The  
 CC compound may in particular be used to treat diseases of the central and  
 CC peripheral nervous systems such as post operative nerve damage, traumatic  
 CC nerve damage, impaired myelination of nerve fibres, conditions resulting  
 CC from a stroke, Parkinson's disease, Alzheimer's disease, dementia,  
 CC sclerosis, nerve degeneration associated with diabetes mellitus,  
 CC disorders affecting the circadian clock or neuro-muscular transmission  
 CC and schizophrenia. Conditions affecting the muscles may also be treated  
 CC with the compound, such as conditions associated with impaired function  
 CC of neuromuscular connections (e.g. genetic or traumatic shock or  
 CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas  
 CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,  
 CC liver and bowel may also be treated using the compound. The compound is  
 CC used in a prosthetic nerve guide, and also to stimulate the ability to  
 CC learn, and to stimulate the memory of a subject.  
 CC Sequence 11 AA:  
 XX

Query Match 85.2%; Score 46; DB 21; Length 11;  
 Best Local Similarity 90.9%; Pred No. 0.057;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 YY 1 ASKKRKNRKA 11  
 DB 1 ASKKRKNRKA 11  
 RESULT 4  
 ID AAY88554  
 XX AAY88554 standard; peptide; 11 AA  
 AC  
 XX AAY88554;  
 XX  
 DT 07-AUG-2000 (first entry)  
 DE NCAM Igl binding peptide 117 used as a control peptide.  
 XX NCAM: neural cell adhesion molecule, Ig1, immunoglobulin domain 1;  
 KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;  
 KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;  
 KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;  
 XX treatment; prosthetic nerve guide; treatment; nervous system.  
 OS  
 XX Synthetic.  
 OS  
 XX WO200018801-A2  
 PN  
 XX 06-APR-2000.  
 PD  
 XX 23-SEP-1999; 99WO-DK00500.  
 PF  
 XX 29-SEP-1999; 99FR-0001332.  
 PR 29-APR-1999; 99PK-0000592.  
 XX (RONN/) RONN L C B.  
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 PA (SORO/) SOROKA V.  
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 PA (BERE/) BEREZIN V.  
 XX Ronn LCB, Rock E, Holm A, Olsen M, OSTERGAARD S, Jensen PH;  
 PI Poulson FM, Soroka V, Ralets I, Berezin V;  
 XX WPI: 2000-293111/25.  
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 PT and Parkinson's diseases -  
 XX Example 5; Fig 7; 11pp; English.  
 XX Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.  
 CC NCAM is found in three forms, two of which are transmembrane forms, while  
 CC the third is attached via a lipid anchor to the cell membrane. All three  
 CC NCAM forms have an extracellular structure consisting five immunoglobulin  
 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the  
 CC N-terminal. The invention relates to a compound containing a peptide  
 CC which binds to the NCAM Igl domain. The compound binds to NCAM-Igl/Ig2  
 CC domain, and is capable of stimulating or promoting neurite outgrowth  
 CC from NCAM presenting cells, and is also capable of promoting the  
 CC proliferation of NCAM presenting cells. The present sequence represents a  
 CC control peptide used in the identification of those binding peptides  
 CC which can be used in the compound. The compound may be used in the  
 CC treatment of normal, degenerated or damaged NCAM presenting cells. The  
 CC compound may in particular be used to treat diseases of the central and

peripheral nervous system such as post operative nerve damage, traumatic nerve injury, acquired cystic fibrosis, Guillain-Barre syndrome, chronic inflammatory demyelinating polyneuropathy, Alzheimer's disease, dementia, Huntington's chorea, Friedreich's ataxia, and diabetes mellitus, and other diseases affecting the circadian clock of nerve-muscular transmission and other chronic conditions affecting the muscles may also be treated with the compound, and conditions associated with impaired function of neurotransmitter systems such as Parkinson's disease, Huntington's chorea, and other diseases affecting the circadian clock of the central nervous system may also be treated with the compound. The compound is used in a method to promote nerve growth, and also to stimulate the ability to learn, and to stimulate the memory of a subject.

24. compound: 11 AA;

Query Match: 100%; Score 46; Db: 21; Length 11;  
Best Local Similarity: 100%; Pred. No. 4.1;  
Matches: 8; Conservative: 2; Indels: 0; gaps: 0;

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XX Neural cell adhesion molecule (NCAM) is a cell-cell adhesion molecule.  
CC NCAM is found in three forms, 1, 2, and 3, of which are transmembrane forms, while  
CC the third is a soluble form. NCAM is involved in cell-cell adhesion, cell-cell  
CC NCAM forms have an extracellular domain, a transmembrane domain, and a cytoplasmic  
CC domain (13 domains). The 13 domains are numbered 1 to 5 from the  
CC N-terminal. The domain 1 is involved in cell-cell adhesion. The domain 2 is  
CC which binds to the NCAM 120 form. The domain 3 binds to NCAM 110/120  
CC form. The domain 4 is involved in cell-cell adhesion. The domain 5 is  
CC involved in cell-cell adhesion. The domain 6 is involved in cell-cell  
CC proliferation of NCAM presenting cells. The present sequence represents a  
CC peptide used in the identification of those binding peptides  
CC which can be used in the compound. The compound may be used in the  
CC treatment of neural, degenerated or damaged NCAM presenting cells. The  
CC compound may be used to treat diseases of the central and  
CC peripheral nervous systems such as post operative nerve damage, traumatic  
CC nerve damage, impaired myelination of nerve fibers, conditions resulting  
CC from a stroke, Parkinson's disease, Alzheimer's disease, dementia,  
CC sclerosis, nerve degeneration associated with diabetes mellitus,  
CC sclerosis affecting the circulation flow of some muscular transmission  
CC and schizophrenia. Conditions affecting the muscles may also be treated  
CC with the compound, such as conditions associated with impaired function  
CC of neurotransmitter systems (e.g., genetic or traumatic stroke of  
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas  
CC (e.g., diabetes mellitus types 1 and 2), kidney (e.g., nephrosis), heart,  
CC liver and bowel may also be treated using the compound. The compound is  
CC used in a method to promote nerve growth, and also to stimulate the ability to  
CC learn, and to stimulate the memory of a subject.

SO Sequence 11 AA;

Query Match: 66.7%; Score 36; Db: 21; Length 11;  
Best Local Similarity: 72.7%; Pred. No. 4.1;  
Matches: 8; Conservative: 2; Indels: 0; gaps: 0;

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XX 04-AUG-1993 (first entry)
DT Mutant HTLV-I residues 88-98, peptide 2L-1.2.
XX Human T-cell leukemia virus, hydrophilic, conjugate, aggregate;
XX diagenesis, antibodies, gp46, mutant, gag; T cell epitope.
XX Synthetic.
XX WO9306843-A.
XX 15-APR-1993.
XX 08-OCT-1992: 92WO-US08405.
XX 08-OCT-1991: 91US-0771553.
XX (UYDU-) UNIV DUKE.
XX Haynes BF, Palker TJ;
XX WPI; 1993-134125/16.
XX Antigenic determinant peptide(s) of HTLV envelope glyco:protein
XX useful for detecting anti-HTLV-I and -II antibodies and as
XX vaccine against HTLV
XX Example 7; Page 32; 50pp; English.
XX To determine which amino acids within the HTLV I envelope amino
XX acids 88-98 were required for absorption of neutralising anti-peptide
XX antibodies to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in
XX which sequential amino acids were each replaced by the amino acid
XX alanine. These 11 mutated peptides, as well as peptide 2L1 bearing the
XX native HTLV-I sequence were tested and identified that amino acids 90,
XX 92, 93 and 95 were important for HTLV-I neutralisation.
XX See also AAR34255-57.
XX
SQ Sequence 11 AA;

```

Query Match 53.7%; Score 29; DB 14; Length 11;  
 Post Local Similarity 71.4%; Field No. 80;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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CY 2 SKPPKN 8
   :|||:|
   :|||:|
Db 2 AKKPNRN 8

```

RESULT 12  
 AAR34255  
 ID AAR34255 standard; peptide; 11 AA.

```

AC AAR34255;
XX 04-AUG-1993 (first entry)
XX Mutant HTLV-I residues 88-98, peptide 2L-1.9.
XX Human T-cell leukemia virus, hydrophilic, conjugate, aggregate;
XX diagenesis, antibodies, gp46, mutant, gag; T cell epitope.
XX Synthetic.
XX WO9306843-A.
XX 15-APR-1993.
XX 08-OCT-1992: 92WO-US08405.
XX 08-OCT-1991: 91US-0771553.
XX

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PA (UYDU-) UNIV DUKE.
XX Haynes BF, Palker TJ;
XX WPI; 1993-134125/16.
XX Antigenic determinant peptide(s) of HTLV envelope glyco:protein
XX useful for detecting anti-HTLV-I and -II antibodies and as
XX vaccine against HTLV
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XX To determine which amino acids within the HTLV-I envelope amino
XX acids 88-98 were required for absorption of neutralising anti-peptide
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XX which sequential amino acids were each replaced by the amino acid
XX alanine. These 11 mutated peptides, as well as peptide 2L-1 bearing the
XX native HTLV-I sequence were tested and identified that amino acids 90,
XX 92, 93 and 95 were important for HTLV-I neutralisation.
XX See also AAR34255-57.
XX
SQ Sequence 11 AA;

```

Query Match 53.7%; Score 29; DB 14; Length 11;  
 Post Local Similarity 71.4%; Field No. 80;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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CY 2 SKPPKN 8
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Db 2 AKKPNRN 8

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RESULT 13  
 AAR34256  
 ID AAR34256 standard; peptide; 11 AA.

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AC AAR34256;
XX 04-AUG-1993 (first entry)
XX Mutant HTLV-I residues 88-98, peptide 2L-1.10.
XX Human T-cell leukemia virus, hydrophilic, conjugate, aggregate;
XX diagenesis, antibodies, gp46, mutant, gag; T cell epitope.
XX Synthetic.
XX WO9306843-A.
XX 15-APR-1993.
XX 08-OCT-1992: 92WO-US08405.
XX 08-OCT-1991: 91US-0771553.
XX (UYDU-) UNIV DUKE.
XX Haynes BF, Palker TJ;
XX WPI; 1993-134125/16.
XX Antigenic determinant peptide(s) of HTLV envelope glyco:protein
XX useful for detecting anti-HTLV-I and -II antibodies and as
XX vaccine against HTLV
XX Example 7; Page 32; 50pp; English.
XX To determine which amino acids within the HTLV-I envelope amino
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XX antibodies to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in
XX which sequential amino acids were each replaced by the amino acid
XX alanine. These 11 mutated peptides, as well as peptide 2L-1 bearing the
XX native HTLV-I sequence were tested and identified that amino acids 90,
XX 92, 93 and 95 were important for HTLV-I neutralisation.
XX See also AAR34255-57.
XX

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GenCode Version 5.14 p5.4578  
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OM protein Protein search using SW model

Run on March 20, 2003, 11:49:50, Search time 16 seconds  
(without alignments)  
66,092 Million cell updates/sec

**Title:** US-09-787-443-1

**Perfect score:** 54

**Sequence:** 1 ASKPPKPNHVA 11

**Scoring table:** PROSUM62  
Gapop 10.0, Gapext 0.5

**Searched:** 293224 seqs, 96134422 residues

**Total number of hits satisfying chosen parameters:** 3883

**Minimum DB seq length:** 0

**Maximum DB seq length:** 20

**Post-processing:** Minimum Match 18  
Maximum Match 100%

**Listing first 45 summaries**

**Database:**  
1: PIR 73: \*  
2: PIR1: \*  
3: PIR2: \*  
4: PIR3: \*  
5: PIR4: \*

Prod No. is the number of results predicted by change to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARYS

Result No.	Score	Query Match Length	ID	Description
1	29	53.7	20 2 S16478	tray protein - Esc
2	25	46.3	17 2 C24166	photosystem II ext
3	24	44.4	20 2 S65746	hypothetical prote
4	24	42.6	6 2 A61140	sperm acrosomal pr
5	23	42.6	13 2 T08593	hypothetical prote
6	23	42.6	13 2 C22905	hypothetical prote
7	23	42.6	13 2 A32971	heparin-binding 1a
8	23	42.6	13 2 C22905	transcription elonga
9	22	40.7	15 2 C22905	hypothetical prote
10	22	40.7	15 2 C22905	protein C24166
11	22	40.7	15 2 C22905	protein kinase (EC
12	22	38.9	14 2 H03778	hypothetical prote
13	21	38.9	14 2 H03778	mixed lymphocyte r
14	21	38.9	14 2 H03778	epsilon receptor he
15	20	37.0	11 2 PH0929	T-cell receptor he
16	20	37.0	11 2 S26801	ribosomal protein
17	20	37.0	11 2 A29144	ribosomal protein
18	20	37.0	11 2 A29144	myosin light chain
19	20	37.0	11 2 A29144	of 11 - phage 7
20	20	37.0	11 2 A29144	hypothetical prote
21	20	37.0	11 2 A29144	hypothetical prote
22	20	37.0	11 2 A29144	labelled 1 leucine
23	20	37.0	11 2 A29144	neurotensin - low
24	20	37.0	11 2 A29144	chaperone, TCP1-re
25	20	37.0	11 2 A29144	cytochrome c oxid
26	20	37.0	11 2 A29144	protein QF200044 -
27	20	37.0	11 2 A29144	casein kinase II (
28	20	37.0	11 2 A29144	T-cell-receptor be
29	20	37.0	11 2 A29144	T-cell receptor be

30	19	35.2	18 2 PS0387	platelet-derived g
31	19	35.2	18 2 A45119	aspartate oxidase I
32	19	35.2	18 2 S16478	agglutinin-type I
33	19	35.2	20 2 A37111	ribulose biphosph
34	19	35.2	20 2 A56046	urinary tract von
35	18	33.3	10 2 A42089	transcription fact
36	18	33.3	11 2 F04267	ribosomal protein
37	18	33.3	12 2 S01222	transcription elonga
38	18	33.3	15 2 S77987	cytochrome c oxid
39	18	33.3	16 2 F44908	chitinase (EC 3.2.
40	18	33.3	16 2 A59155	multicystatin - 10
41	18	33.3	18 2 A78660	glucuronidase
42	18	33.3	18 2 S45373	translation elonga
43	18	33.3	19 2 B16592	lactate dehydrogen
44	18	33.3	20 2 S28405	lamin B receptor -
45	18	33.3	20 2 F05557	arabinoside acti

#### ALIGNMENTS

##### RESULT 1

S16478  
tray protein - Escherichia coli plasmid incFV (fragment)

C/Species: Escherichia coli

C/Date: 13-Mar-1997 #sequence\_revision 15 Apr-1997 #text\_change 11-Apr-1997

C/Accession: S16478

F,di Laurence, L., Frost, L.S., Finlay, B.B., Fairclough, W.

Mol Microbiol. 5: 1779-1790, 1991

A/Title: Characterization of the oriT region of the incFV plasmid pND208.

A/Reference number: S16478, M01D 1204497, PMID 1341709

A/Accession: S16478

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-20 <Lau>

A/Cross-references: EMBL:X59611

C/Genetics:

A/Genome: plasmid incFV

Query Match

Best local similarity 53.7%; Score 29; DB 2; Length 20;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 3 KKPKNRK 10

2 KKPKNRK 9

1 KKPKNRK 8

0 KKPKNRK 7

0 KKPKNRK 6

0 KKPKNRK 5

0 KKPKNRK 4

0 KKPKNRK 3

0 KKPKNRK 2

0 KKPKNRK 1

0 KKPKNRK 0

0 KKPKNRK -1

0 KKPKNRK -2

0 KKPKNRK -3

0 KKPKNRK -4

0 KKPKNRK -5

0 KKPKNRK -6

0 KKPKNRK -7

0 KKPKNRK -8

0 KKPKNRK -9

0 KKPKNRK -10

0 KKPKNRK -11

0 KKPKNRK -12

0 KKPKNRK -13

0 KKPKNRK -14

0 KKPKNRK -15

0 KKPKNRK -16

0 KKPKNRK -17

0 KKPKNRK -18

0 KKPKNRK -19

0 KKPKNRK -20

0 KKPKNRK -21

0 KKPKNRK -22



QY 3 KKKENIK 9  
| | | |  
| | | |  
Db 8 KKKPHVNI 14

## RESULT 9

D28551

Hypothetical protein 4 - Streptococcus mutans (strain GS-5) (fragment)

C:Species: Streptococcus mutans

C:Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 15-Oct-1999

C:Accession: D28551

R:Shirota, T.; Katsube, H.K.

J. Bacteriol. 170, 419-426, 1992

A:Title: Sequence analysis of the Streptococcus mutans fructosyltransferase gene and the

A:Reference number: A1937, with 441184, F01233325

A:Accession: D28551

A:Molecule type: DNA

A:Residues: 1-15 &lt;STO&gt;

A:Cross-references: GB:M18954, NID:915375, PIRN:AAA89961, P10 J1067227

Query Match 40.7%; Score 22; DB 2; Length 12;

Best Local Similarity 45.5%; Pred. No. 7 1e+03;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASKPPENIK 11  
| | | | |  
| | | | |  
Db 2 ANKKIRIRIK 12

## RESULT 10

PT0082

Fruit-in Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 07-Feb-1996 #sequence\_revision 19-Apr-1996 #text\_change 06-Jun-1997

C:Accession: PT0082

R:Ragusa, A.; Kato, M.; Kawakami, M.; Ohts, Y.

submitted to JIPID, December 1995

A:Description: Two dimensional electrophoresis of plant proteins and standardization of

A:Reference number: PNU013

A:Accession: PT0082

A:Molecule type: Protein

A:Residues: 1-15 &lt;STO&gt;

A:Experimental source: leaf

Query Match 40.7%; Score 22; DB 2; Length 15;

Best Local Similarity 45.5%; Pred. No. 8 7e+02;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASKPPENIK 11  
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| | | | |  
Db 1 ATIKPKLIXA 11

## RESULT 11

I45957

Protein kinase (EC 2.7.1.37), cAMP-dependent, type I-alpha regulatory chain - bovine (fr

C:Species: Bos primigenius taurus (cattle)

C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 18-Jun-1999

C:Accession: I45957

R:Lee, D.C.; Carmichael, D.F.; Krebs, E.G.; McKnight, G.S.

Proc. Natl. Acad. Sci. U.S.A. 80, 3509-3512, 1983

A:Title: Isolation of a cDNA clone for the type I regulatory subunit of bovine cAMP-depe

A:Reference number: I45957; NCID:83221645, PMID:6190178

A:Accession: I45957

A:Status: preliminary, translated from GR/EMBL/DD84

A:Molecule type: mRNA

A:Residues: 1-19 &lt;LEED&gt;

A:Cross-references: D2:K23233, NID:915375, PIRN:AAA30706.1; EMBL:63364

C:Superfamily: cAMP-dependent protein kinase regulatory chain, cAMP receptor protein cyd

C:Keywords: phosphotransferase

Query Match 40.7%; Score 22; DB 2; Length 19;

Best Local Similarity 57.1%; Pred. No. 1 1e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKKENIK 10  
| | | |  
| | | |  
Db 2 KAKTNVK 8

## RESULT 12

H83778

Hypothetical protein BHI032 (imported) - Bacillus halodurans (strain C 125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 19-Jun-2001

C:Accession: H83778

R:Ragusa, A.; Katsube, H.; Takaki, Y.; Maeno, S.; Sasaki, P.; Yasui, M.; Fujii, E.; et al

Nucleic Acids Res. 28, 4217-4231, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A8150, NCID:30555923, F01233322

A:Accession: H83778

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-14 &lt;STO&gt;

A:Cross-references: GB:AP001510, GP:EA000004, NID:9153440, PIRN:BAE17701, S010:0001

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BHI032

Query Match 38.9%; Score 21; DB 2; Length 14;

Best Local Similarity 80.0%; Pred. No. 1 3e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KKKPK 7  
| | | |  
| | | |  
Db 2 KKKPK 6

## RESULT 13

PX0031

mixed lymphocyte reaction inhibitor - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 24-Feb-1993

C:Accession: PX0031

R:Shimizu, T.; Ohara, T.; Wada, N.; Omeri, A.; Kamada, N.

J. Biochem. 107, 435-439, 1990

A:Title: Rat liver arginase suppresses mixed lymphocyte reaction.

A:Reference number: PX0031; NCID:90256720, PMID:2140155

A:Accession: PX0031

A:Molecule type: protein

A:Residues: 1-15 &lt;SHT&gt;

A:Experimental source: liver

C:Keywords: lymphocyte

Query Match 38.9%; Score 21; DB 2; Length 15;

Best Local Similarity 80.0%; Pred. No. 1 4e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SKKPK 6  
| | | |  
| | | |  
Db 8 SKKPK 12

## RESULT 14

A61220

epilium receptor modulating protein (EC 3.4.21. ) mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 21-Mar-1996

C:Accession: A61220

R:Matsumura, S.; Tazaki, D.H.

Cell Immunol. 137, 252-259, 1991

A:Title: The murine epilium receptor modulating protein: a novel serine protease which me

A:Reference number: A61220, NCID:3156570, PMID:1679381

A:Accession: A61220

A:Molecule type: protein

A:Residues: 1-18 &lt;MAP&gt;

Comment: This serine protease from a T cell hybridoma does not reduce levels of CD23 expression in hybridized serine protease.

### Keywords:

Cherry Mall 11 14.98; Score 21; DB 2; Length 18;  
14.98; Score 21; DB 2; Length 18;  
14.98; Score 21; DB 2; Length 18;

[illegible]

А. С. КИРИЛЕНКО

4 Alpha-1,4-hexA

	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
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[illegible]

$\frac{d}{dt} \left( \frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$

**Figure 1**

Diagram illustrating the experimental setup for measuring the effect of temperature on the rate of reaction between hydrogen peroxide and potassium iodide.

The diagram shows two test tubes labeled A and B, each containing a solution of hydrogen peroxide and potassium iodide. The test tubes are placed in water baths at different temperatures: Test Tube A is in a cold water bath, and Test Tube B is in a warm water bath. The reaction is initiated by adding a catalyst (potassium iodide) to the hydrogen peroxide solution. The rate of reaction is measured by observing the time taken for the formation of a precipitate or gas.

EX-117, 1457

[illegible]
$$A_i^* M_i = 1 \text{ for } i = 1, \dots, n \quad \text{and} \quad Y_i = \min A_i^* N A_i$$

Year	Age	Sex	Location	Species	Number	Notes
1971	10	M	...	...	...	...
1972	11	F	...	...	...	...
1973	12	M	...	...	...	...
1974	13	F	...	...	...	...
1975	14	M	...	...	...	...
1976	15	F	...	...	...	...
1977	16	M	...	...	...	...
1978	17	F	...	...	...	...
1979	18	M	...	...	...	...
1980	19	F	...	...	...	...
1981	20	M	...	...	...	...
1982	21	F	...	...	...	...
1983	22	M	...	...	...	...
1984	23	F	...	...	...	...
1985	24	M	...	...	...	...
1986	25	F	...	...	...	...
1987	26	M	...	...	...	...
1988	27	F	...	...	...	...
1989	28	M	...	...	...	...
1990	29	F	...	...	...	...
1991	30	M	...	...	...	...
1992	31	F	...	...	...	...
1993	32	M	...	...	...	...
1994	33	F	...	...	...	...
1995	34	M	...	...	...	...
1996	35	F	...	...	...	...
1997	36	M	...	...	...	...
1998	37	F	...	...	...	...
1999	38	M	...	...	...	...
2000	39	F	...	...	...	...
2001	40	M	...	...	...	...
2002	41	F	...	...	...	...
2003	42	M	...	...	...	...
2004	43	F	...	...	...	...
2005	44	M	...	...	...	...
2006	45	F	...	...	...	...
2007	46	M	...	...	...	...
2008	47	F	...	...	...	...
2009	48	M	...	...	...	...
2010	49	F	...	...	...	...
2011	50	M	...	...	...	...
2012	51	F	...	...	...	...
2013	52	M	...	...	...	...
2014	53	F	...	...	...	...
2015	54	M	...	...	...	...
2016	55	F	...	...	...	...
2017	56	M	...	...	...	...
2018	57	F	...	...	...	...
2019	58	M	...	...	...	...
2020	59	F	...	...	...	...
2021	60	M	...	...	...	...
2022	61	F	...	...	...	...
2023	62	M	...	...	...	...
2024	63	F	...	...	...	...
2025	64	M	...	...	...	...
2026	65	F	...	...	...	...
2027	66	M	...	...	...	...
2028	67	F	...	...	...	...
2029	68	M	...	...	...	...
2030	69	F	...	...	...	...
2031	70	M	...	...	...	...
2032	71	F	...	...	...	...
2033	72	M	...	...	...	...
2034	73	F	...	...	...	...
2035	74	M	...	...	...	...
2036	75	F	...	...	...	...
2037	76	M	...	...	...	...
2038	77	F	...	...	...	...
2039	78	M	...	...	...	...
2040	79	F	...	...	...	...
2041	80	M	...	...	...	...
2042	81	F	...	...	...	...
2043	82	M	...	...	...	...
2044						

1.  $\mathcal{F} = \mathcal{F}^{\text{reg}} \cup \mathcal{F}^{\text{sing}}$ , where  $\mathcal{F}^{\text{reg}}$  is the set of regular functions and  $\mathcal{F}^{\text{sing}}$  is the set of singular functions.

# 2025 Year-End Survey

[illegible]

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG). The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG).

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GenCore version 5.1.4.F5.4578  
Copyright 1997-2003 GenCore Inc.

ON file: filein search, using sw model

Run: March 20, 2003, 09:40:06, Search time: 11 seconds  
(without alignments)

41,476 Million total updates/sec

Title: US-09-787-443-1

Sequence: 1 ASKREPENIKA 11

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Search: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1147

Minimum PR seq length: 0

Maximum PR seq length: 20

Post-processing: Minimum March 08

Maximum March 1998

Listing first 45 summaries

Database: SwissProt\_40\*

Result No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	Hit	Description
1	29	63.7	23	TRYS_ECOLI
2	24	49.1	14	PS19_PWB
3	24	48.4	14	HE_COTJA
4	21	38.9	20	PS19_PWB
5	20	47.0	4	844E_EB01
6	20	47.0	11	CS1E_BACD
7	20	37.0	11	MCH_MACE
8	19	35.2	16	MMPX_SOUT
9	19	35.2	16	ALLI_CAMA
10	19	35.2	19	MIFH_TRIP
11	19	35.2	20	ACRH_BOVIN
12	18	33.3	10	COX2_PAVT
13	18	33.3	14	PS19_PWB
14	18	33.3	14	PS19_PWB
15	18	33.3	14	PS19_PWB
16	18	33.3	14	PS19_PWB
17	18	33.3	14	PS19_PWB
18	18	33.3	14	PS19_PWB
19	18	33.3	14	PS19_PWB
20	18	33.3	14	PS19_PWB
21	18	33.3	14	PS19_PWB
22	18	33.3	14	PS19_PWB
23	18	33.3	14	PS19_PWB
24	18	33.3	14	PS19_PWB
25	18	33.3	14	PS19_PWB
26	18	33.3	14	PS19_PWB
27	18	33.3	14	PS19_PWB
28	18	33.3	14	PS19_PWB
29	18	33.3	14	PS19_PWB
30	18	33.3	14	PS19_PWB
31	18	33.3	14	PS19_PWB
32	18	33.3	14	PS19_PWB
33	18	33.3	14	PS19_PWB

34	16	29.6	12	1	SO1E_BACSU
35	16	29.6	13	1	BLAC_STROR
36	16	29.6	14	1	PS19_PWB
37	16	29.6	15	1	ACERACTIA
38	16	29.6	16	1	ONC1_ONSMY
39	16	29.6	17	1	PS19_PWB
40	16	29.6	18	1	COX2_THRSE
41	16	29.6	19	1	PS19_PWB
42	16	29.6	20	1	PS19_PWB
43	16	29.6	21	1	PS19_PWB
44	16	29.6	22	1	PS19_PWB
45	16	29.6	23	1	PS19_PWB

## ALIGNMENTS

RESULT 1	TRYS_ECOLI	STANDARD;	PRT;	20 AA.
ID	TRYS_ECOLI			
AC	PS19_PWB			
DT	01-FEB-1994 (Prl 28, Created)			
DT	01-FEB-1994 (Prl 33, Last sequence update)			
DT	01-FEB-1994 (Prl 33, Last annotation update)			
DE	Tray protein (Fragment).			
OS	Tray.			
OS	Escherichia coli			
OC	Plasmid IncV pBD208.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia.			
OX	NCBI_TaxId=562;			
FN	[1]			
PP	SEQUENCE FROM N A			
PA	MENTINE.204497, PubMed:1943709;			
PA	di Laurentio L, Frost L S, Finlay B R, Paranchych W;			
RT	"Characterization of the first region of the IncV plasmid pBD208."			
PL	Mol Microbiol 5:1779-1790(1991).			
CC	FOR THE EXCHANGE OF PLASMID DNA IT IS ALSO RESPONSIBLE FOR			
CC	CONJUGAL DNA METABOLISM. TRAY IS REQUIRED FOR STAMIN-SPECIFIC			
CC	WORKING AT GRI, THE TRANSFER OF OTHER PLASMIDS.			
CC	-1- SWISS-PROT entry is available. It is provided through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
CC	at the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its copyright is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
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CC	or send an email to <a href="mailto:license@sib-sb.ch">license@sib-sb.ch</a> ).			
CC	EMBL: X56411; CAA4176.1; -			
DP	PIR: S16478; S16478			
PA	PS19_PWB			
RT	MENTINE.204497, PubMed:1943709;			
CC	FOR THE EXCHANGE OF PLASMID DNA IT IS ALSO RESPONSIBLE FOR			
CC	CONJUGAL DNA METABOLISM. TRAY IS REQUIRED FOR STAMIN-SPECIFIC			
CC	WORKING AT GRI, THE TRANSFER OF OTHER PLASMIDS.			
CC	-1- SWISS-PROT entry is available. It is provided through a collaboration			
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PA	PS19_PWB			
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CC	EMBL: X56411; CAA4176.1; -			
DP	PIR: S16478; S16478			
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CC	EMBL: X56411; CAA4176.1; -			
DP	PIR: S16478; S16478			
PA	PS19_PWB			
RT	MENTINE.204497, PubMed:1943709;			
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DP	PIR: S16478; S16478			
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[illegible]

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Matches 15; Conservative 9; Mismatches 2; Indels 0; Gaps 0
QY 1 ASPPRP 7
   |||||
DB 9 ARAKPP 15

RESULT 4
PGK PACEE
ID PGK_PACEE STANDARD; PRT; 20 AA.
AC PRG325
DT 16-OCT-2001 (Rel. 40, Created)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
BT 15 JUN-2002 (Rel. 41, Last annotation update)
DE Phosphoglycerate kinase (EC 2.7.2.3) (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID:1396;
RN (1)
RT SEQUENCE, AND INDUCTION.
RC STRAIN-NCIMP_11796;
FA Brown N., Dowds P.C.A.;
FI Submitted Apr. 2001; 15 hrs since first data built.
CC 1. CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate > ADP + 1-phospho-D-glyceroyl phosphate.
CC -1. PATHWAY: Second phase of glycolysis; second step.
CC -2. STEPWISE LOCATION: Cytoplasmic.
CC -3. STRAINAGE LOCATION: Cytoplasmic.
CC -4. INDUCTION: By heat shock.
CC -5. SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
DP Inferred; IPRO1876; PKR.
DR PROSITE; PS0011; POLYPHOSPHATE KINASE; PARTIAL.
EK Transferase; kinase; Glycolysis; Heat shock.
FT NON TER
SQ REFERENCE 20 AA; 2403 MW; EFMZCAPI1550153 CR664;

Query Match 38.9%; Score 21; DB 1; length 20;
Best Local Similarity 50.0%; Pred. No. 5,3e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0
QY 2 STEPPPT 9
   |||||
DB 2 MKKSIPNV 9

RESULT 5
B4AK_PORGI
ID B4AK_PORGI STANDARD; PRT; 8 AA.
AC PB1886;
DT 30-MAY-2000 (Rel. 39, Created)
DI 30 MAY-2000 (rel 39, last sequence update)
BT 10 MAY 2000 (rel 39, last annotation update)
DE 44 kDa immunogenic protein (fragment).
CD F ribonuclease junctional "nucleotides 3'UTR" (185);
CO Baculovirus; Revertebrates; Arthropods; Revertebrates;
CC Escherichia coli; Filiphomonas.
CX NCBI_TaxID:817;
RN (1)
RT SPOUNCE.
RC STRAIN-VPB_3492;
FA Morris J.M., Lowe D.N.;
FI "Sequenced by reference of cDNA from whole cell antisense of rat foetus polyoma virus (J93A15.1)".
FI Vet. Microbiol. 21:37-44(2000).
CC -1. SIMILARITY: TO P-GALACTAN HEMAGGLUTININ A.
KW Antigen.
FT NON TER
SQ SEQUENCE 8 AA; 980 MW; 0654-1442-06A76D (90664);

Query Match 37.0%; Score 20; DB 1; length 8;
Best Local Similarity 100.0%; Pred. No. 1,1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

OY 6 KPN1 9  
 ||||  
 Db 5 KPN1 9

## RESULT 6

CSIS\_BACSU  
 ID CSIS\_BACSU STANDARD; PRT; 11 AA.

DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-2002 (Rel. 41, Last annotation update)  
 DE Cold shock protein CSIS (11 kDa cold shock protein) (Fragment).  
 OS Bacillus subtilis.  
 CC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus  
 NC NCBI\_TaxID=1423;  
 RN (1)

FP SEQUENCE  
 RA STEIN-19 / 74642;  
 RA Graumann P, Schroeder V, Schmid P, Marchiel M A;  
 PL Submitted (OCT-1997) to the SWISS-PROT data bank  
 RN (2)  
 RP CHARACTERIZATION:  
 RP STRAIN=169 / 74642;  
 RA MEDLINE=96345629; PubMed=8755892;  
 RA Graumann P, Schroeder V, Schmid P, Marchiel M A;  
 RT Cold shock stress-induced proteins in Bacillus subtilis";  
 PL Bacteriol 178:4411-4419(1996)

CT 1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC 1- LOCATION: IN REFERENCE TO LOW TEMPERATURE  
 FT NON TER 11  
 SQ SEQUENCE 11 AA; 1360 MW; 1687956470330 CRC64;

Query Match 37.0%; Score 20; DB 1; Length 11;  
 Best Local Similarity: 100.0%; Pred No 4 Cons;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 RNK1 10  
 ||||  
 Db 2 RNK1 5

## RESULT 7

MDH\_ACIDE  
 ID MDH\_ACIDE STANDARD; PRT; 17 AA.

AC PRO540;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-OCT-2001 (Rel. 40, Last annotation update)  
 DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).  
 GN MDH.

OS Acidovorax delafeldii  
 CC Bacteria; Proteobacteria; beta subphylum; Gammaproteobacteria;  
 CC Acidovorax  
 CC NCBI\_TaxID=47330;  
 RN (1)  
 RP SEQUENCE:  
 RP STRAIN=CCUG 12929;  
 RA MEDLINE=97334132; PubMed=9190829;

RT "Structural studies of malate dehydrogenases (MDHs): MDHs in  
 RT Freundimonas species are the first reported MDHs in Proteobacteria  
 RT which resemble lactate dehydrogenases in primary structure.";  
 DT Bacteriol. 179:4066-4070(1997).

CC 1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) -> oxaloacetate + NADH.  
 CC 1- SIMILARITY: BELONGS TO THE MDH FAMILY MDH SUBFAMILY.  
 CC Interpro: Ippro1350; MDH  
 CC PROSITE: PS00064; MDH; PARTIAL:  
 KW Oxidoreductase; Transaminase; MDH  
 FT NON TER 17  
 SQ SEQUENCE 17 AA; 1662 MW; 1108111616902 CRC64;

Query Match 37.0%; Score 20; DB 1; Length 17;  
 Best Local Similarity: 80.0%; Pred. No. 7e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 KKPPE 7  
 ||||  
 Db 2 KKPPE 6

## RESULT 8

IMPX\_SOLTU  
 ID IMPX\_SOLTU STANDARD; PRT; 16 AA.

AC PR0501;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Unidentified mitochondrial matrix protein (Fragment).  
 OS Solanum tuberosum (Potato).  
 CC Eukaryota; Viridiplantae; Streptophyta; Etrypophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots;  
 CC Asteridae; Euasteride I; Solanales; Solanaceae; Solanum.  
 CC NCBI\_TaxID=4113;  
 RN (1)

RP SEQUENCE:  
 RP TISSUE=Tuber;  
 RA MEDLINE=97077345; PubMed=8910910;  
 RA Wansch I, Kruff V, Schmitz H V, Braun H P;  
 RT "New insights into the composition, molecular mass and stoichiometry  
 RT of the protein complexes of plant mitochondria.";  
 PL Plant J. 9:357-368(1996).

CC 1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 KM Mitochondrion.  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1768 MW; C58D4DB48A18B8D CRC64;

Query Match 35.0%; Score 19; DB 1; Length 16;  
 Best Local Similarity: 40.0%; Pred No 1e+03;  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 ASKKRNK1 10  
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 Db 1 ASNVKELVE 10

## RESULT 9

AL13\_CARMA  
 ID AL13\_CARMA STANDARD; PRT; 18 AA.

AC P81816;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinus statin 13.

OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;  
 CC Malacostraca; Eumalacostraca; Decapoda; Decapoda; Decapoda;  
 CC Eucyprina, Eucyprina; Foulonidae; Foulonidae; Carcinus.  
 CC NCBI\_TaxID=6759;  
 RN (1)

RP SEQUENCE:  
 RP TISSUE=Cerebral ganglion, and thoracic ganglion;  
 RA MEDLINE=9811133; PubMed=9461295;  
 RA DIVE H, Johnson A H, Maestre J L, Scott A G, Jaro P P,  
 RA Thorpe A;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 DT Eur. J. Biochem. 250:727-734(1997).

CC 1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC 1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC Neuropeptide; Amidation; Malicene family.  
 KW MOD RES 18  
 FT MOD RES 18  
 SQ SEQUENCE 18 AA; 2265 MW; 3511108160A27 CRC64;

Query Match: 35.28; Score 19; DB 1; Length 19;  
 Best Local Similarity: 57.1%; Pred. No. 1,3e+03;  
 Matches: 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

4 KRPENK 10  
 1 KPDQAIK 7

RESULT 12  
 ID COXO\_PABIT STANDARD; PRT; 10 AA.  
 DT 01-OCT-1994 (rel. 30; Created)  
 DT 01-OCT-1994 (rel. 30; Last sequence update)  
 DT 15-MAY-2000 (rel. 41; Last annotation update)  
 DE Cytosolic - alpha 5-type II vit. D-receptor (EC 1.9.3.1)  
 DE (Fragment).  
 DE COX8.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eumetazoa; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID:9986;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart, and Liver;  
 FA Friend F., Radnath B., to the Swiss Spot 4th Day,  
 PI Submitted (Mar-1994) to the Swiss Spot 4th Day,  
 CC FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR DOPED POLYPEPTIDE  
 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL CYTOCHROME IN  
 MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 ferredoxin:NADH + H<sup>+</sup> oxidoreductase  
 (EC 1.1.1.13).  
 CC -2- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE WITH FAMILY.  
 KW Oxidoreductase; Mitochondrion.  
 FT NCN TER 10 10  
 SQ SEQUENCE 10 AA; 197 MW; 2795440279399 CPO64;

Query Match: 35.28; Score 19; DB 1; Length 19;  
 Best Local Similarity: 57.1%; Pred. No. 1,3e+03;  
 Matches: 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

4 KRPENK 10  
 1 KPDQAIK 7

RESULT 13  
 ID RS19\_CLOPP STANDARD; PRT; 14 AA.  
 DT 30-MAY-2000 (rel. 35; Created)  
 DT 10-MAY-2000 (rel. 39; Last sequence update)  
 DT 10-MAY-2000 (rel. 39; Last annotation update)  
 DE 300 ribosomal protein S19 (Fragment).  
 GN RPS19 OR RPS19.  
 OS Clostridium perfringens phytoplasm.

Query Match: 35.28; Score 19; DB 1; Length 20;  
 Best Local Similarity: 57.1%; Pred. No. 1,3e+03;  
 Matches: 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

4 KRPENK 10  
 1 KPDQAIK 7

RESULT 12  
 ID COXO\_PABIT STANDARD; PRT; 10 AA.  
 DT 01-OCT-1994 (rel. 30; Created)  
 DT 01-OCT-1994 (rel. 30; Last sequence update)  
 DT 15-MAY-2000 (rel. 41; Last annotation update)  
 DE Cytosolic - alpha 5-type II vit. D-receptor (EC 1.9.3.1)  
 DE (Fragment).  
 DE COX8.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eumetazoa; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID:9986;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart, and Liver;  
 FA Friend F., Radnath B., to the Swiss Spot 4th Day,  
 PI Submitted (Mar-1994) to the Swiss Spot 4th Day,  
 CC FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR DOPED POLYPEPTIDE  
 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL CYTOCHROME IN  
 MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 ferredoxin:NADH + H<sup>+</sup> oxidoreductase  
 (EC 1.1.1.13).  
 CC -2- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE WITH FAMILY.  
 KW Oxidoreductase; Mitochondrion.  
 FT NCN TER 10 10  
 SQ SEQUENCE 10 AA; 197 MW; 2795440279399 CPO64;

Query Match: 35.28; Score 19; DB 1; Length 10;  
 Best Local Similarity: 57.1%; Pred. No. 1,3e+03;  
 Matches: 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

4 KRPENK 10  
 1 KPDQAIK 7

RESULT 13  
 ID RS19\_CLOPP STANDARD; PRT; 14 AA.  
 DT 30-MAY-2000 (rel. 35; Created)  
 DT 10-MAY-2000 (rel. 39; Last sequence update)  
 DT 10-MAY-2000 (rel. 39; Last annotation update)  
 DE 300 ribosomal protein S19 (Fragment).  
 GN RPS19 OR RPS19.  
 OS Clostridium perfringens phytoplasm.



CC Bacteria; Firmicutes; Mollicutes; Achaeplastatales;  
 CC Achaeplastatales; Phytolasma.  
 CC NCBI\_TaxID=35776;  
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 CC SEQUENCE FROM N.A.  
 CC MEDLINE=9435090; PubMed=8071198;  
 CC Gundersen D.E., Lee I.M., Rehner S.A., Davis P.F., Kingsbury D.T.;  
 CC "Phylogeny of mycoplasma-like organisms (phytoplasmatales), a basis for  
 CC their classification";  
 CC RT Bacteriol. 176:5244-5254(1994).  
 CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY  
 CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).  
 CC -1- SIMILARITY: RELATES TO THE S19 FAMILY OF RIBOSOMAL PROTEINS.  
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 CC EMBL: L27011; AAA9394.1;  
 CC InterPro: IPR002222; PIR00001\_S19;  
 CC EC0017; PIR00001; PIR00001; PIR00001; PARTIAL.  
 CC PIR00001; PIR00001; PIR00001;  
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 CC SEQUENCE 14 AA; 1642 MW; 200478B9FFFEA8 CRC64;  
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 CC Best Local Similarity 44.4%; Pred. No 1.4e+03;  
 CC Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
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 CC QY 2 SKPPENIK 10  
 CC :|||  
 CC Db 5 AKGDKKXK 13  
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 CC RESULT 14  
 CC ID RS19\_LUMEP STANDARD; PRT; 14 AA.  
 CC AC Q48878;  
 CC DT 30-MAY-2000 (Rel. 39, Created)  
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 CC DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 CC DE 10S ribosomal protein S19 (fragment).  
 CC OS PIR00001; PIR00001;  
 CC PIR00001; PIR00001; PIR00001;  
 CC Locofah w/ches; -broom phytoplasmatales.  
 CC Bacteria; Firmicutes; Mollicutes; Achaeplastatales;  
 CC Achaeplastatales; Phytolasma.  
 CC NCBI\_TaxID=35773;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=9435090; PubMed=8071198;  
 CC Gundersen D.E., Lee I.M., Rehner S.A., Davis P.F., Kingsbury D.T.;  
 CC "Phylogeny of mycoplasma-like organisms (phytoplasmatales), a basis for  
 CC their classification";  
 CC RT Bacteriol. 176:5244-5254(1994).  
 CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY  
 CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).  
 CC -1- SIMILARITY: RELATES TO THE S19 FAMILY OF RIBOSOMAL PROTEINS.  
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 CC EC0017; PIR00001; PIR00001; PIR00001; PARTIAL.  
 CC PIR00001; PIR00001; PIR00001;  
 CC NON\_TER 1 1  
 CC SEQUENCE 14 AA; 1642 MW; 200478B9FFFEA8 CRC64;

KW Ribosomal protein; rRNA-binding.  
 FT NON\_TER 1  
 SQ SEQUENCE 14 AA; 1642 MW; 200478B9FFFEA8 CRC64;  
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 CC Query Match 33.3%; Score 18; DB 1; Length 14;  
 CC Best Local Similarity 44.4%; Pred. No 1.4e+03;  
 CC Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
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 CC QY 2 SKPPENIK 10  
 CC :|||  
 CC Db 5 AKGDKKXK 13  
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 CC RESULT 15  
 CC ID COXI\_THUOB STANDARD; PRT; 15 AA.  
 CC AC P80978;  
 CC DT 01-NOV-1997 (Rel. 35, Created)  
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 CC DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 CC DE Cytochrome c oxidase polypeptide VIC-2 (EC 1.9.3.1) (Fragments).  
 CC OS Thunnus obesus (Bigeye tuna).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 CC Acanthomorpha; Acanthopterygii; Perccomorphia; Perciformes; Scombroidei;  
 CC Scombridae; Thunnus.  
 CC NCBI\_TaxID=8241;  
 CC [1]  
 CC SEQUENCE  
 CC RP TISSUE=Heart;  
 CC RC MEDLINE=97454291; PubMed=9310366;  
 CC PA Arnold S., Lee I., Kim M., Song F., Liner P., Lottersch F.,  
 CC RA Kadenbach B.;  
 CC RT "The subunit structure of cytochrome c oxidase from tuna heart and  
 CC liver"; Biochem. 248:99-103(1997).  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 ferroxycytochrome c + O2 = 4 ferrioxycytochrome c + 2 H2O.  
 CC CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC KM oxidoreductase; inner membrane; Mitochondrion.  
 CC FT NON\_TER 1 1  
 CC FT NON\_CONS 8 9  
 CC FT NON\_TER 15 15  
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 CC Job time : 14 secs





1 NTER (1991) seq1.  
 2 111  
 3 SEQUENCE:  
 4 METATRE (0604594) RefMod 966699;  
 5 34380000; Blamberg L, Prusik M, Grollman P,  
 6 "Identification and characterization of the human dehydrogenase from  
 7 *Leishmania* and its homologues".  
 8 EMBL/GenBank/ DDBJ: J01311 (199005).  
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    Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0
CY  3 KKKPNK 10
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DB  4 EKPEKKV 11

RESULT 5
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AC  O9TR21;
DT  01-MAY-2000 (TRENBLER), 13. Created)
DT  01-MAY-2000 (TRENBLER), 13. Last sequence update)
DT  01-JUN-2000 (TRENBLER), 14. Last annotation update)
DE  Pleiotrophin (Fragment).
OS  Sus scrofa (pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Carnivordia; Sus.
CX  NCBI_Taxid=9823;
RN  [1]
RP  SEQUENCE.
EX  MEDLINE=3616377, PubMed=8568456;
FA  Brigstock D.R., Kim G.Y., Steffen C.L.;
RT  "pig uterine luminal fluid contains the developmentally regulated
RT  neurotrophic factor, pleiotrophin."
PL  J. Endocrinol. 149:103-111(1996).
SQ  SEQUENCE: 17 AA: 1378 MW: 52475857/517400 070647
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    Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0
CY  3 KKKPNK 10
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DB  4 EKPEKKV 11

RESULT 6
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DT  01-MAY-2000 (TRENBLER), 13. Created)
DT  01-MAY-2000 (TRENBLER), 13. Last sequence update)
DT  01-JUN-2000 (TRENBLER), 14. Last annotation update)
DE  Osteoblast-specific factor 1 (Fragment).
OS  Homo sapiens (Human).
CX  PubMed=1534747, Medline=1534747;
OC  Eukaryota; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Carnivora; Primates; Haplorhina;
OC  NCBI_Taxid=9606;
RN  [1]
RP  SEQUENCE.
EX  MEDLINE=1534747, PubMed=1534747;
FA  Takamatsu H., Itoh M., Kimura M., Ohsigatawara D., Amano F.;
RT  "Expression and purification of biologically active human OGF 1 in
RT  Escherichia coli."
RL  Escherichia coli.
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CY  3 KKKPNK 10
    :|:::|
DB  4 EKPEKKV 11

RESULT 7

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FT NON TER 1
SQ SEQUENCE 10 AA: 1167 MW: 406A97771A32763 CRC64;

Query Match
Best Local Similarity 40.7% Score 22; DB 12; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 KRPK 6
DB 2 KRPK 5

RESULT 14
Query Match
Best Local Similarity 40.7% Score 22; DB 12; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 KRPK 6
DB 2 KRPK 5

RESULT 15
Query Match
Best Local Similarity 40.7% Score 22; DB 12; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 KRPK 6
DB 2 KRPK 5

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FT NON TER 1
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 KRPK 6
DB 2 KRPK 5

RESULT 14
Query Match
Best Local Similarity 40.7% Score 22; DB 12; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 KRPK 6
DB 2 KRPK 5

RESULT 15
Query Match
Best Local Similarity 40.7% Score 22; DB 12; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 KRPK 6
DB 2 KRPK 5

```

Thu Mar 20 13:48:45 2003

us-09-787-443-1.rpt

Page 5

db 2 KPR 5

Search completed: March 20, 2003, 08:42:53  
Job time : 30 secs





GenCore version 5.1.4 ps 4578  
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OM protein - protein search, using sw model

Run on: March 20, 2003, 09:41:01, Search time 15 seconds

(without alignments) 21 577 Million cell updates/sec

Title: US-09-787-443-1

Perfect score: 54

Sequence: 1 ASKPPKPN1KA 11

Scoring table: BLOSUM62

Gapop 10 0, Gapext 0 5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 133970

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	33	61.1	11	1	US-08-116-733-31
2	29	53.7	11	1	US-08-116-733-1
3	29	53.7	11	1	US-08-116-733-32
4	29	53.7	11	1	US-08-116-733-39
5	29	53.7	11	1	US-08-116-733-48
6	29	53.7	11	1	US-08-116-733-41
7	29	53.7	13	1	US-08-116-733-30
8	28	51.9	9	1	US-08-116-733-45
9	28	51.9	11	1	US-08-116-733-36
10	28	51.9	11	2	US-08-856-661 9
11	28	51.9	11	2	US-08-197-521 16
12	28	51.9	11	1	US-08-434-122 104
13	28	51.9	18	4	US-09-465 325-102
14	28	51.9	18	4	US-09-115-737-103
15	28	51.9	19	1	US-09-556 823-5
16	27	50.0	15	3	US-08-041-899-17
17	27	50.0	15	3	US-08-837-058-17
18	27	50.0	18	2	US-08-841-483-15
19	27	50.0	18	2	US-08-841-483-16
20	27	50.0	19	4	US-09-382-911-15
21	27	50.0	19	4	US-09-382-911-16
22	27	50.0	20	2	US-08-488-210A-29
23	27	50.0	20	2	US-08-329 206-29
24	27	50.0	20	2	US-08-498 209B-28
25	27	50.0	20	2	US-08-408 611-28
26	27	50.0	20	2	US-08-934 222-85
27	26	48.1	9	2	US-08-933-402-85

29	26	48.1	9	2	US-09-297 621 85	Sequence 87, Appl
30	26	48.1	9	2	US-08-532 818 85	Sequence 88, Appl
31	26	48.1	9	3	US-09-231-797-85	Sequence 89, Appl
32	26	48.1	9	3	US-08-934-224 85	Sequence 90, Appl
33	26	48.1	9	4	US-08-933 843-85	Sequence 91, Appl
34	26	48.1	9	4	US-08-934-223-85	Sequence 92, Appl
35	26	48.1	9	4	US-09-413-492-85	Sequence 93, Appl
36	26	48.1	10	1	US-08-401-512-57	Sequence 94, Appl
37	26	48.1	15	2	US-08-466-860-13	Sequence 95, Appl
38	26	48.1	15	2	US-08-472 242A-13	Sequence 96, Appl
39	26	48.1	15	4	US-08-276-776-13	Sequence 97, Appl
40	26	48.1	17	4	US-08-471 209-13	Sequence 98, Appl
41	26	48.1	17	4	US-08-101-751A-42	Sequence 99, Appl
42	26	48.1	18	2	US-08-894 329-4	Sequence 100, Appl
43	26	48.1	18	4	US-08-306-044-4	Sequence 101, Appl
44	25	46.3	15	3	US-08-641-889-18	Sequence 102, Appl
45	25	46.3	15	3	US-08-837-058-18	Sequence 103, Appl
			20	4	US-09-242-221A-1	Sequence 104, Appl

## ALIGNMENTS

RESULT 1  
US-08-116-733-31

Sequence 31, Application US/08116733

Patent No. 5516632

GENERAL INFORMATION:

APPLICANT: PALMER, Thomas J.

APPLICANT: HAYNES, Barton F.

TITLE OF INVENTION: SYNTHETIC PEPTIDES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESS: NIXON & VANCEPHE P.C.

STREET: 1100 NORTH GREEK ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/116,733

FILING DATE: 07-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1573-33

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 203737 NIXN UR

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-116-733-31

Query Match

Best local similarity 61.1%; Score 33; DB 1; Length 11;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASKPPKPN 8

DE 1 ATKPPKPN 8



Db 2 TKKPNRN 8

## RESULT 5

US-08-116-733-40

Sequence 40, Application US/08116733

Patent No. 5516632

GENERAL INFORMATION:

APPLICANT: PALKER, Thomas J.

APPLICANT: HAYNES, Barton F.

TITLE OF INVENTION: SYNTHETIC PEPTIDES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/116,733

FILING DATE: 07-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1579-33

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-116-733-40

Query Match 53.7%; Score 29; DB 1; Length 11;

Best Local Similarity 71.4%; Pred. No. 27;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 2 TKKPNRN 8

## RESULT 6

US-08-116-733-41

Sequence 41, Application US/08116733

Patent No. 5516632

GENERAL INFORMATION:

APPLICANT: PALKER, Thomas J.

APPLICANT: HAYNES, Barton F.

TITLE OF INVENTION: SYNTHETIC PEPTIDES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/116,733

FILING DATE: 07-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1579-33

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-116-733-41

Query Match 53.7%; Score 29; DB 1; Length 11;

Best Local Similarity 71.4%; Pred. No. 27;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 2 TKKPNRN 8

## RESULT 7

US-08-116-733-30

Sequence 30, Application US/08116733

Patent No. 5516632

GENERAL INFORMATION:

APPLICANT: PALKER, Thomas J.

APPLICANT: HAYNES, Barton F.

TITLE OF INVENTION: SYNTHETIC PEPTIDES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/116,733

FILING DATE: 07-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1579-33

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-116-733-30

Query Match 53.7%; Score 29; DB 1; Length 13;



INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-856-663-8

Query Match 51.9% Score 28, DB 1, Length 11,  
Best Local Similarity 62.5%, Pred. No. 41,  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KKKRNIK 9  
||||:|  
Dh 1 KKKRNIK 8

RESULT 11  
US-08-193-521-10  
Sequence 10, Application US/08434120  
Patent No. 5696563  
GENERAL INFORMATION:  
APPLICANT: Maloy, W. Lee  
APPLICANT: Kari, U. Prasad  
APPLICANT: Williams, Jon I.  
TITLE OF INVENTION: Biologically Active Peptide  
TITLE OF INVENTION: Compositions and Uses Therefor  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gillfillan,  
ADDRESSEE: Cecchi & Stewart  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: DM4 V2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/193,521  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/870,960  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 421250-161  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: May be a C-terminal amide,  
OTHER INFORMATION: and/or may be acetylated at  
OTHER INFORMATION: N-terminus.  
US-08-193-521-10

Query Match 51.9% Score 28, DB 1, Length 18;  
Best Local Similarity 62.5%, Pred. No. 66;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 3 KKKRNIK 10  
||||:|  
Dh 9 KKKRNIK 16

RESULT 12  
US-08-434-120-104  
Sequence 104, Application US/08434120  
Patent No. 5635479  
GENERAL INFORMATION:  
APPLICANT: Baker, Margaret A.  
APPLICANT: Jacob, Leonard S.  
APPLICANT: Maloy, W. Lee  
TITLE OF INVENTION: Treatment of Gynecological  
TITLE OF INVENTION: Malignancies with  
TITLE OF INVENTION: Biologically Active Peptides  
NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gillfillan,  
ADDRESSEE: Cecchi & Stewart  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: DM4 V2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/434,120  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,950  
FILING DATE:  
APPLICATION NUMBER: US/08/226,108  
FILING DATE:  
APPLICATION NUMBER: US/07/937,462  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 421250-194  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-434-120-104

Query Match 51.9% Score 28, DB 1, Length 18;  
Best Local Similarity 62.5%, Pred. No. 66;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KKKRNIK 10  
||||:|  
Dh 9 KKKRNIK 16

RESULT 13  
US-08-465-325-103  
Sequence 103, Application US/08465325  
Patent No. 5696563  
GENERAL INFORMATION:



TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 323-5870  
 TELEFAX: (415) 854-0875  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-556-823-5

Query Match 51.98; Score 28; DB 1; Length 19;  
 Best Local Similarity 71.48; Pred. No. 79;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 4 KPPNIX 10  
 ||| : :  
 Db 1 KPTNMX 7

Search completed: March 20, 2003, 03:43:41  
 Job time : 17 secs





GenCore version 5.1.4-p5\_4578  
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OW protein - protein search, using sw model

Run on: March 20, 2003, 09:41:41 : Search time 13 seconds  
(without alignments)

45,237 Million cell updates/sec

US-09-787-443-1  
Perfect score: 54  
Sequence: 1 ASKPRPNIKA 11

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 22153 seqs, 53462247 residues

Total number of hits satisfying chosen Parameters: 45299

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

# Database :

## Published Applications A1\*

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3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB pep.\*  
4: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
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13: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB pep.\*  
14: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB pep.\*

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	61.1	13	10	US-09-730-772-10
2	33	61.1	13	10	US-09-735-849-10
3	28	51.9	9	9	US-10-094-699-44
4	26	48.1	15	9	US-10-092-750-39
5	26	48.1	17	9	US-09-929-724-42
6	25	46.3	20	10	US-09-844-813-11
7	25	46.3	20	10	US-10-057-812-15
8	24	44.4	9	10	US-09-566-193A-15
9	24	44.4	10	9	US-10-108-798-12
10	24	44.4	10	12	US-10-040-332-47
11	24	44.4	14	9	US-09-821-861-11
12	24	44.4	14	12	US-10-041-030-17
13	24	44.4	16	10	US-09-736-059A-29
14	24	44.4	20	9	US-09-742-096-16
15	24	44.4	20	9	US-09-510-332-58
16	24	44.4	20	10	US-09-765-527-114
17	24	44.4	20	10	US-09-844-761-34491
18	24	44.4	20	10	US-09-841-132-230
19	24	44.4	20	10	US-09-841-132-231

20	24	44.4	20	10	US-09-841-132-230	Sequence 210, App
21	24	44.4	20	10	US-09-841-132-231	Sequence 211, App
22	23	42.6	9	10	US-09-796-1234-54	Sequence 24, App1
23	23	42.6	9	10	US-09-872-922-34	Sequence 34, App1
24	23	42.6	15	10	US-09-884-267A-7	Sequence 21, App1
25	23	42.6	16	9	US-08-424-552P-27	Sequence 217, App
26	23	42.6	17	10	US-09-864-761-41554	Sequence 41554, A
27	23	42.6	18	9	US-07-809-331-630	Sequence 630, App
28	23	42.6	18	12	US-10-113-573-2	Sequence 2, App1
29	23	42.6	20	9	US-09-736-457-1834	Sequence 1834, Ap
30	23	42.6	20	9	US-09-052-241-1834	Sequence 1834, Ap
31	23	42.6	20	9	US-09-849-626-1834	Sequence 1834, Ap
32	23	42.6	20	10	US-09-841-132-232	Sequence 1834, Ap
33	23	42.6	20	10	US-09-839-184-10	Sequence 182, App
34	23	40.7	5	9	US-09-912-165A-50	Sequence 50, App1
35	23	40.7	7	9	US-08-178-286-13	Sequence 13, App1
36	22	40.7	7	9	US-09-861-257-13	Sequence 13, App1
37	22	40.7	7	10	US-09-883-642A-12	Sequence 12, App1
38	22	40.7	9	10	US-09-796-294-35	Sequence 15, App1
39	22	40.7	10	9	US-09-114-293-3	Sequence 3, App1
40	22	40.7	11	9	US-09-929-724-76	Sequence 28, App1
41	22	40.7	11	9	US-10-108-795-28	Sequence 28, App1
42	22	40.7	11	9	US-10-044-995-3	Sequence 3, App1
43	22	40.7	11	10	US-09-839-666-12	Sequence 12, App1
44	22	40.7	11	10	US-09-873-676-16	Sequence 16, App1
45	22	40.7	11	10	US-09-941-611-3	Sequence 3, App1

## ALIGNMENTS

RESULT 1  
US-09-730-772-10  
Sequence 10, Appl  
Patent No. US20010011131A1  
GENERAL INFORMATION:  
APPLICANT: Luyten, Frank P.  
APPLICANT: Moos, Jr., Malcolm  
APPLICANT: Chang, Steven Chao-Huan  
TITLE OF INVENTION: CAPTILASE-DERIVED M.EPHROGENETIC  
NUMBER OF SEQUENCES: 24  
REFERENCE ADDRESS:  
ADDRESSEE: Knudsen, Matens, Olson & Bear  
STREET: 620 Newport Center Drive, 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION NUMBER: US-09-730-772  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/836,081  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bartfeld, Neil S  
REGISTRATION NUMBER: 39,901  
REFERENCE/POCKET NUMBER: N/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-235-8550  
TELEFAX: 619-235-0176  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid

RESEARCHER: I have a question about the results of the study. I don't understand why the results are so different from the other studies. Can you explain that to me?

Journal of Management Education 33(1) pp. 107-120  
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10.1177/0095647209342562  
http://jme.sagepub.com  
hosted at  
http://online.sagepub.com

1. **Abstract**

1. *Applied Statistics*, 35/5975, 849

AFFILIANT, SAYING, BUREAU  
 AFFILIANT, MOORE, ST., MALCOLM  
 AFFILIANT, BART, STATION CHURCH  
 AFFILIANT, N. AFFILIANT, SERVICES, MORPHOGENETIC

MEMBER OF SEQUENT EST. 24  
 CORPORATION OF AMERICA  
 ANDERSON, FRODO, MITCHELL, JAMES & BOA

1. NAME: Stewart, David  
 2. SEX: M  
 3. BIRTHDATE: 11/11/44  
 4. BIRTHPLACE: N.Y.C.  
 5. PRESENT ADDRESS: 300 E. 77th St.  
 6. CITY: New York, N.Y.  
 7. STATE: N.Y.  
 8. ZIP: 10021

MODEL TYPE: DISKLESS  
 MEMORY: 16M (expandable)  
 OPERATING SYSTEM: WINDOWS

"SPRING AIRCRAFT N. DATA."  
APPROXIMATE NUMBER OF COPIES  
FILMED DATE:  
ACQUISITION:

THE AUTHOR(S) AND/OR  
APPLYING NUMBER: 0000-0001,  
PLANT NAME:  
ADDRESS/AREA OF ORIGIN:

REGISTRATION NUMBER: 39,901  
FREQUENT/DO NOT NUMBER: NHH099,001and  
TELECOMMUNICATIONS IN THE PAST 24

1      **PRETEXT:**    9/15/2000 07:17  
2      **PRETEXT:**  
3      **INFORMATION FOR SFO TO MIA:** 10:  
4      **RE: JENNER, JARARAH/RENTON:**

1. **NAME:** STEFAN STANISLAW  
 2. **DATE:** 1990-01-10  
 3. **TIME:** 14:00  
 4. **LOCATION:** 100-100-100  
 5. **REMARKS:** 100-100-100  
 6. **SIGNATURE:** 100-100-100  
 7. **DATE:** 1990-01-10  
 8. **TIME:** 14:00  
 9. **LOCATION:** 100-100-100  
 10. **REMARKS:** 100-100-100  
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 13. **TIME:** 14:00  
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 42. **DATE:** 1990-01-10  
 43. **TIME:** 14:00  
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 47. **DATE:** 1990-01-10  
 48. **TIME:** 14:00  
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 52. **DATE:** 1990-01-10  
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 57. **DATE:** 1990-01-10  
 58. **TIME:** 14:00  
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 61. **SIGNATURE:** 100-100-100  
 62. **DATE:** 1990-01-10  
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 67. **DATE:** 1990-01-10  
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 72. **DATE:** 1990-01-10  
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 77. **DATE:** 1990-01-10  
 78. **TIME:** 14:00  
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 87. **DATE:** 1990-01-10  
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 98. **TIME:** 14:00  
 99. **LOCATION:** 100-100-100  
 100. **REMARKS:** 100-100-100

[illegible][illegible][illegible]

Publication No. 20000200467014A  
GENERAL INFORMATION:  
APPLICANT: SIMARD, John, J.L.  
APPLICANT: DIAMOND, David, G  
FIELD OF INVENTION: NOT KNOWN

FILE NUMBER: 015A  
TITLE OF INVENTION: CANCER  
FILE PREFERENCE: OTLMM 015A  
CURRENT ATTORNEY NUMBER: 00000094,699  
CURRENT FILING DATE: 2002-06-21

PRIOR FILING DATE: 2001-03-07  
NUMBER OF SEQ ID NOS: 109  
SOFTWARE: FASTSEQ for Windows Version 4.0

TYPE: prt  
ORGANISM: Homo sapien  
S-10-094-699.44

Twenty match	81.4%	Score 26	DB 3	Length 7
Best Local Similarity	71.4%	Pred. No. 2e+05		
Matches	5	Conservative	1	Mismatches
				Indels

2. ПРИНЦИП 8

Sequence 39, Application US/100  
Publication No. US2003032257A1

APPLICANT: Hammond, Philip W.  
APPLICANT: Alpin, Julia  
APPLICANT: Wright, Martin C.

FILE REFERENCE: 6036705000  
 ORIGINATING AGENCY NUMBER: 000  
 CURRENT FILING DATE: 2004-03  
 BUREAU AFFILIATION NUMBER: 000

NUMBER OF SEQ ID NOS: 253  
SOFTWARE: FASTSEQ FOR WINDOWS  
SEQ ID NO: 9

TYPE: PRT  
ORGANISM: Homo sapiens  
S-10-092-750-39

```

Query Match      40.18;
Best Local Similarity 72.48;
Matches      5; Conservative

```

3 AKKOSKPN 9

RESULT 5  
 S-09-999-724 42  
 Sequence 42, Application US/09  
 Publication No. US20030022355A1

APPLICANT: WICKHAM, THOMAS J.  
APPLICANT: KOVESDI, IMRE  
APPLICANT: BROUGH, DOUGLAS E

FILE REFERENCE - 212960  
CURRENT APPLICATION NUMBER -  
CURRENT FILING DATE - 2001.10  
DEPOSITED WITH - NUMBER -

PRIOR FILING DATE: 1957-01-29

PRIOR APPLICATION NUMBER: US 09/053,150  
 PRIOR FILING DATE: 1996-11-27  
 PRIOR APPLICATION NUMBER: US 09/050,946  
 PRIOR FILING DATE: 1996-09-21  
 PRIOR APPLICATION NUMBER: US 08/771,124  
 PRIOR FILING DATE: 1996-08-21  
 PRIOR APPLICATION NUMBER: US 08/563,268  
 PRIOR FILING DATE: 1995-11-28  
 NUMBER OF SEQ ID NOS: 94  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 42  
 LENGTH: 17  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic  
 US-09-000-724-42

Query Match 48.1% Score 26; DB 9; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 1,3e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0

Cy 1 AKKPKPK 10  
 Db 2 AKKPKPKPK 11

RESULT 6  
 US-09-776-724A-252

Sequence 252, Application US/09776724A  
 Publication No. US2003050455A1  
 GENERAL INFORMATION:  
 APPLICANT: Rosen et al.  
 TITLE OF INVENTION: 64 Human Secreted Proteins  
 FILE REFERENCE: P2011  
 CURRENT APPLICATION NUMBER: US/09-776-724A  
 CURRENT FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-08  
 PRIOR APPLICATION NUMBER: 09/776,789  
 PRIOR FILING DATE: 2000-09-26  
 PRIOR APPLICATION NUMBER: 09/022,982  
 PRIOR FILING DATE: 1999-01-14  
 PRIOR APPLICATION NUMBER: 07/713,447  
 PRIOR FILING DATE: 1998-07-15  
 PRIOR APPLICATION NUMBER: 09/052,661  
 PRIOR FILING DATE: 1997-07-15  
 PRIOR APPLICATION NUMBER: 09/052,972  
 PRIOR FILING DATE: 1997-07-16  
 PRIOR APPLICATION NUMBER: 60/052,971  
 PRIOR FILING DATE: 1997-07-16  
 PRIOR APPLICATION NUMBER: 60/072,974  
 PRIOR FILING DATE: 1997-07-16  
 PRIOR APPLICATION NUMBER: 60/052,973  
 PRIOR FILING DATE: 1997-07-16  
 PRIOR APPLICATION NUMBER: 60/054,870  
 PRIOR FILING DATE: 1997-07-16  
 PRIOR APPLICATION NUMBER: 60/052,875  
 PRIOR FILING DATE: 1997-07-16  
 PRIOR APPLICATION NUMBER: 60/053,440  
 PRIOR FILING DATE: 1997-07-22  
 PRIOR APPLICATION NUMBER: 60/056,359  
 PRIOR FILING DATE: 1997-08-18  
 PRIOR APPLICATION NUMBER: 60/055,725  
 PRIOR FILING DATE: 1997-08-18  
 PRIOR APPLICATION NUMBER: 60/055,985  
 PRIOR FILING DATE: 1997-09-19  
 PRIOR APPLICATION NUMBER: 60/055,952  
 PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/055,985  
 PRIOR FILING DATE: 1997-08-18  
 PRIOR APPLICATION NUMBER: 60/055,351  
 PRIOR FILING DATE: 1997-08-18  
 PRIOR APPLICATION NUMBER: 60/055,156  
 PRIOR FILING DATE: 1997-08-18  
 PRIOR APPLICATION NUMBER: 60/055,724  
 PRIOR FILING DATE: 1997-08-18  
 PRIOR APPLICATION NUMBER: 60/055,946  
 PRIOR FILING DATE: 1997-08-18  
 PRIOR APPLICATION NUMBER: 60/055,683  
 PRIOR FILING DATE: 1997-08-18  
 NUMBER OF SEQ ID NOS: 294  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 252  
 LENGTH: 20  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-776 724A-252

Query Match 45.3% Score 25; DB 9; Length 20;  
 Best Local Similarity 55.0%; Pred. No. 2,3e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0

Cy 3 KKKPKPK 11  
 Db 11 KKKPKPK 19

RESULT 7  
 US-09-844-813-1

Sequence 1, Application US/09844813  
 Patent No. US20020042135A1  
 GENERAL INFORMATION:  
 APPLICANT: Nakanishi, Mahito  
 APPLICANT: Nagoshi, Emi  
 APPLICANT: Akutsu, Teruo  
 APPLICANT: Takeda, Katsuo  
 APPLICANT: Hasegawa, Mamoru  
 TITLE OF INVENTION: FLAVR WITH NUCLEAR LOCALIZATION SIGNAL  
 FILE REFERENCE: 50026/015001

CURRENT APPLICATION NUMBER: US/09/844,813  
 CURRENT FILING DATE: 2001-04-27  
 PRIOR FILING DATE: 2000-07-06  
 PRIOR APPLICATION NUMBER: 09/242,131  
 PRIOR FILING DATE: 1996-12-27  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 1  
 LENGTH: 20  
 TYPE: PRT  
 ORGANISM: Simian Virus 40  
 US-09-844-813-1

Query Match 46.3% Score 25; DB 10; Length 20;  
 Best Local Similarity 53.3%; Pred. No. 2,3e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Cy 1 AKKPK 6  
 Db 15 AKKPK 20

RESULT 8  
 US 10-057-812-15

Sequence 15, Application US/10057812  
 Publication No. US20020197619A1  
 GENERAL INFORMATION:  
 APPLICANT: Nikiforov, Theo T.  
 TITLE OF INVENTION: Kinase Assays Using Polycations  
 FILE REFERENCE: 100/07930  
 CURRENT APPLICATION NUMBER: US/10/057,812



US-10-042-202-47

Query Match 44.4% Score 24; DB 12; Length 10;

Best Local Similarity 57.1%; Pred. No. 1.8e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 3 KKPENI 9

DB 4 KKPENI 10

RESULT 12

US-09-821-861-11

Sequence 11, Application US/09821861

Patent No. US2003023171A1

GENERAL INFORMATION:

APPLICANT: Schoof, Thomas C.

APPLICANT: Cao, Ximeng

TITLE OF INVENTION: METHODS OF IDENTIFYING AGENTS THAT

FILE REFERENCE: A94 47, 132,435,003e2

CURRENT APPLICATION NUMBER: US/09/821,861

PRIORITY FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 14

TYPE: PRT

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: Synthetic Peptide

US-09-821-861-11

Query Match

Best Local Similarity 44.4% Score 24; DB 9; Length 14;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

CY 3 KKPENI 11

DB 4 KKPENI 12

RESULT 13

US-10-041-030-17

Sequence 17, Application US/10041030

Patent No. US2003015034A1

GENERAL INFORMATION:

APPLICANT: Powers, Scott

APPLICANT: Mu, David

APPLICANT: Xiang, Phil

APPLICANT: Peng, Yue

APPLICANT: Tuladik Inc.

TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Mammalian

FILE REFERENCE: 018761-00681005

CURRENT APPLICATION NUMBER: US/10/041,030

PRIORITY FILING DATE: 2001-12-28

PRIOR APPLICATION NUMBER: US 60/259,503

PRIORITY FILING DATE: 2001-01-02

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 17

LENGTH: 14

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: amino acid

OTHER INFORMATION: sequence identity in comparison of pellino 1 and

OTHER INFORMATION: pellino 2

US-10-041-030-17

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 3 KKPENI 8

DB 1 KKPENI 6

RESULT 14

US-09-736-959A-28

Sequence 28, Application US/09736959A

Patent No. US20020076415A1

GENERAL INFORMATION:

APPLICANT: University of Southern California

APPLICANT: Xu, Jinhong

TITLE OF INVENTION: HEPATITIS C VIRUS GENE PRODUCTS

FILE REFERENCE: 13761-742

CURRENT APPLICATION NUMBER: US/09/736,959A

PRIORITY FILING DATE: 2000-12-14

PRIOR APPLICATION NUMBER: US 60/170,835

PRIORITY FILING DATE: 1999-12-14

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 16

TYPE: PRT

ORGANISM: Hepatitis C Virus (HCV-1 subtype)

US-09-736-959A-28

Query Match

Best Local Similarity 44.4% Score 24; DB 10; Length 16;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 3 KKPENI 8

DB 9 KKPENI 14

RESULT 15

US-09-742-096-16

Sequence 16, Application US/09742096

Patent No. US20020155441A1

GENERAL INFORMATION:

APPLICANT: DROTHER, PIERRE

APPLICANT: DAUBERSTES, PIERRE

TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES

FILE REFERENCE: 200773US001V

CURRENT APPLICATION NUMBER: US/09/742,096

PRIORITY FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 08/973,642

PRIORITY FILING DATE: 1998-02-06

PRIOR APPLICATION NUMBER: PCT/FR00/00394

PRIORITY FILING DATE: 1996-06-12

PRIOR APPLICATION NUMBER: FR 95/07007

PRIORITY FILING DATE: 1995-06-13

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 16

LENGTH: 20

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Peptide

US-09-742-096-16

Query Match

Best Local Similarity 44.4% Score 24; DB 9; Length 20;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 3 KKPENI 9

DB 6 KKPENI 12

Thu Mar 20 13:48:44 2003

us-09-787-443-1.rabb

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